

CLAIMS

1. A reaction mixture, comprising:
 - a) a first oligonucleotide primer comprising i) a sequence corresponding to a promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, and iv) a sequence coding for a first epitope marker; and
 - b) a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker.
2. The reaction mixture of Claim 1, further comprising:
 - c) template.
3. The reaction mixture of Claim 2, wherein said first oligonucleotide primer further comprises v) a region of complementarity to said template.
4. The reaction mixture of Claim 2, wherein said second oligonucleotide primer further comprises iii) a region of complementarity to said template.
5. The reaction mixture of Claim 3, wherein said region of complementarity is greater than 15 bases in length.
6. The reaction mixture of Claim 4, wherein said region of complementarity is greater than 15 bases in length.
7. The reaction mixture of Claim 1, wherein second epitope marker is selected from the group consisting of SEQ ID NOS: 5, 6, 7, 8 and 9.
8. The reaction mixture of Claim 2, wherein said template comprises a region of a gene, said gene selected from the group consisting of the APC gene, the NF1 gene, the NF2 gene, the BRCA1 gene and the BRCA2 gene.

9. A kit, comprising:
 - a) a first oligonucleotide primer comprising i) a sequence corresponding to a promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, and iv) a sequence coding for a first epitope marker; and
 - b) a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker.
10. The kit of Claim 9, wherein said first oligonucleotide primer further comprises v) a region of complementarity to a template.
11. The kit of Claim 9, wherein said second oligonucleotide primer further comprises iii) a region of complementarity to a template.
12. The kit of Claim 10, wherein said region of complementarity is greater than 15 bases in length.
13. The kit of Claim 11, wherein said region of complementarity is greater than 15 bases in length.
14. The kit of Claim 9, wherein second epitope marker is selected from the group consisting of SEQ ID NOS: 5, 6, 7, 8 and 9.
15. The kit of Claim 10, wherein said template comprises a region of a gene, said gene selected from the group consisting of the APC gene, the NF1 gene, the NF2 gene, the BRCA1 gene and the BRCA2 gene.
16. A method of introducing coding sequence for epitope markers into nucleic acid, comprising:
 - a) providing:

- i) a first oligonucleotide primer comprising i) a sequence corresponding to a promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, and iv) a sequence coding for a first epitope marker;
 - ii) a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker;
 - iii) a polymerase; and
 - iv) template; and
 - b) mixing said template with said first primer, second primer and said polymerase under conditions such that amplified template is produced, said amplified template coding for said first and second epitope markers.
17. The method of Claim 16, wherein said first oligonucleotide primer further comprises v) a region of complementarity to said template.
 18. The method of Claim 16, wherein said second oligonucleotide primer further comprises iii) a region of complementarity to said template.
 19. The method of Claim 17, wherein said region of complementarity is greater than 15 bases in length.
 20. The method of Claim 18, wherein said region of complementarity is greater than 15 bases in length.
 21. The method of Claim 16, wherein second epitope marker is selected from the group consisting of SEQ ID NOS: 5, 6, 7, 8 and 9.
 22. The method of Claim 16, wherein said template of step (a) comprises a region of a gene, said gene selected from the group consisting of the APC gene, the NF1 gene, the NF2 gene, the BRCA1 gene and the BRCA2 gene.

23. The method of Claim 22, wherein said template further comprises a sequence coding for an affinity marker.
24. A method, comprising:
- a) providing:
 - i) the amplified template of Claim 22;
 - ii) a misaminoacylated tRNA comprising an affinity marker; and
 - iii) a translation system; and
 - b) introducing said amplified template and said misaminoacylated tRNA into said translation system under conditions such that said affinity marker is incorporated into a nascent protein in a reaction mixture, whereby said nascent protein comprises 1) said first epitope marker, 2) said second epitope marker, and 3) said affinity marker.
25. The method of Claim 24, wherein said translation system is a cell-free translation system.
26. The method of Claim 25, wherein said cell-free translation system is selected from the group consisting of *Escherichia coli* lysates, wheat germ extracts, insect cell lysates, rabbit reticulocyte lysates, frog oocyte lysates, dog pancreatic lysates, human cell lysates, mixtures of purified or semi-purified translation factors and combinations thereof.
27. The method of Claim 24, wherein said affinity marker comprises a biotinyl moiety.
28. The method of Claim 24, wherein said misaminoacylated tRNA comprises BODIPY-FL-lysyl-tRNA.
29. The method of Claim 24, further comprising, after step b), step c) adding an antibody reactive with said second epitope marker.

30. The method of Claim 29, wherein said antibody is reactive with an epitope sequence selected from the group consisting of a HIS-tag, a C-myc-tag, a FLAG-tag, a STREP-tag, and an HA-tag.
31. A method, comprising:
- a) providing:
 - i) the amplified template of Claim 23; and
 - iii) a translation system;
 - b) introducing said amplified template into said translation system under conditions such that a nascent protein is produced, said nascent protein comprising 1) said first epitope marker, 2) said second epitope marker, and 3) said affinity marker; and
 - c) separating said nascent protein from said translation system using said affinity marker.
32. The method of Claim 31, wherein said translation system is a cell-free translation system.
33. The method of Claim 32, wherein said cell-free translation system is selected from the group consisting of *Escherichia coli* lysates, wheat germ extracts, insect cell lysates, rabbit reticulocyte lysates, frog oocyte lysates, dog pancreatic lysates, human cell lysates, mixtures of purified or semi-purified translation factors and combinations thereof.
34. The method of Claim 31, wherein said affinity marker comprises a third epitope marker.
35. The method of Claim 31, further comprising after step (c): d) analyzing for the presence of said first epitope marker and said second epitope marker.

36. The method of Claim 31, further comprising, after step (c): d) adding an antibody reactive with said second epitope marker.
37. The method of Claim 36, wherein said antibody is reactive with an epitope sequence selected from the group consisting of a HIS-tag, a C-myc-tag, a FLAG-tag, a STREP-tag, and an HA-tag.